REMARKS

Claim 4 has been objected to based on a minor typographical error. The claim has been amended accordingly. Withdrawal of the objection is respectfully requested.

Claims 1-12 stand rejected under 35 U.S.C. §112, second paragraph, as failing to particularly point out and distinctly claim the subject matter. Specifically, the rejection states that the recitation of a polynucleotide encoding amino acids from about 1 to about 529, or an isolated nucleic acid from about 2 to about 2468 is indefinite.

In the interest of advancing prosecution Claims 1, 2, 4 and 6 have been amended and Claims 3 and 5 have been cancelled without prejudice or disclaimer and without acquiescing to the rejections. The claims have been amended to explicitly recite particular sequences or structures having clearly defined relationships to them. The Sequence Listing of the Applicants' specification discloses the particular polynucleotide recited in the claims. Based on this disclosure, one skilled in the art can immediately apprehend those sequences that are the complement of or 90% identical thereto. In view of this sequence data, the metes and bounds of the rejected claims can be readily determined.

Based on the forgoing, the Applicants respectfully submit that the amended claims are definite. Accordingly, withdrawal of the rejection of Claims 1-12 under 35 U.S.C. §112, second paragraph is respectfully requested.

Claims 1, 6, 8-12, 23 and 24 stand rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement. Specifically, the rejection asserts that the specification fails to teach a representative number of species of the genus of polynucleotides encompassed by the claims so as to adequately suggest that the inventors were in full possession of the claimed invention at the time of filing.

The Applicants respectfully submit that one skilled in the art would appreciate that the Applicants were in full possession of the claimed subject matter at the time of filing. SEQ ID NO:2 explicitly sets forth the complete amino acid sequence encoded by the polynucleotide of element (a) in Claim 1. Further, at paragraph [0043], the specification clearly states that the polynucleotide can be the complement of or at least 90% identical to SEQ ID NO:2.

The Applicants further respectfully assert that the specification clearly identifies a polynucleotide that encodes SEQ ID NO:2 as the BRCC-3 gene. Thus, a claim reciting "BRCC-3" is fully supported by the written description. However, the Applicants have amended Claim 23 to recite antisense oligonucleotides to the BRCC-3 gene, which encodes the amino acid sequence contained in SEQ ID NO:2.

In light of the Sequence Listing and the written description provided in the specification, one skilled in the art would understand that the Applicants were in full possession of the claimed invention at the time of filing. Thus, withdrawal of the rejection of the claims under 35 U.S.C. §112, first paragraph, is respectfully requested.

Claims 1-7 stand rejected under 35 U.S.C. §102(a) as anticipated by Acc. No. AF303178, which discloses the polynucleotide encoding SEQ ID NO: 2 and polynucleotide subsequences thereof.

The Applicants respectfully submit that the submission and sequence information described in Acc. No. AF303178 is not prior art. The sequence information was submitted to GenBank on September 5, 2000 in confidence, and was not released into the public domain until after the Applicants' priority date of April 06, 2001. The attached e-mail correspondence between GenBank and the first named inventor verifies that Acc. No. AF303178 was not released until after the effective filing date of the application.

In accordance with MPEP §2128, a publication is available as prior art only upon a sufficient showing that such document has been disseminated or otherwise made available to the extent that interested persons can exercise reasonable diligence to locate it. In an analogous case, it was held that a printed mailing prepared prior to an application's filing date did not constitute prior art because it was not mailed until after the filing date and there was no evidence that any addressees had received the publication earlier than the postmark date. *Carella v. Starlight Archery*, 804 F2d 135, 231 USPQ 644 (Fed. Cir. 1986).

As the sequence submission was unavailable until after the April 2001 filing of the underlying provisional application, Acc. No. AF303178 does not constitute prior art under 35 U.S.C. §102(a). Accordingly, the Applicants respectfully request withdrawal of the rejection of Claims 1-7 in view of this submission.

Claims 1, 3-7 and 23 stand rejected under 35 U.S.C. 102(a) as being allegedly anticipated by Ota. The rejection states that Acc. No. AX878198 (SEQ ID NO: 13103) of Ota. teaches a polynucleotide encoding amino acids 2-259 of SEQ ID NO:2, polynucleotide subsequences thereof, and antisense oligonucleotides thereof.

The sequence identified as Acc. No. AX878198 is a truncated sequence which is missing the last 61 amino acids of the BRCC3 gene of SEQ ID NO:2. Consequently, the sequence of Acc. No. AX878198 does not disclose the entire polynucleotide sequence encoding the amino acid sequence contained in SEQ ID NO: 2. Furthermore, the described sequence is sufficiently truncated that the sequence of Acc. No. AX878198 does not disclose a polynucleotide that is 90% identical to the presently claimed molecule. Claims 1, 3-7 and 23 are thus not anticipated by Ota and withdrawal of the rejection under 35 U.S.C. 102(a) is respectfully requested.

Claims 1-7 stand rejected under 35 U.S.C. 102(b) as being anticipated by Williams. Specifically, the rejection states that Acc. No. AAA00789 of Williams teaches polynucleotides comprising between 2-2468 contiguous nucleotides of SEQ ID NO: 1, or encoding from about 1 to about 529 amino acids of SEQ ID NO:2.

The Applicants respectfully submit that the sequence identified by Acc. No. AAA00789 in the alignment data provided by the Examiner is a truncated form of the gene, including only 285 nucleotides encoding 95 amino acids. Consequently, Williams does not disclose a polynucleotide sequence encoding the amino acid sequence contained in SEQ ID NO: 2, a complement thereof, or a polynucleotide that is 90% identical to the molecule recited in Claims 1-7. Accordingly, the Applicants respectfully request withdrawal of the rejection under 35 U.S.C. 102(b).

Claim 23 stands rejected under 35 U.S.C. 102(a)/103(a) as allegedly anticipated by or obvious over Schlegel. The rejection asserts that Schlegel teaches an antisense oligonucleotide, specifically Acc. No AAH66886, that targets SEQ ID NO:1. The rejection further asserts that the Applicants have the burden of establishing whether the polynucleotide identified by Acc. No AAH66886 has the function of inhibiting gene expression.

The Applicants respectfully submit that Schlegel does not disclose a molecule that one skilled in the art would reasonably expect to function as an antisense to the BRCC-3 gene of SEQ ID NO:2. Indeed, the text of Schlegel makes no mention of the BRCC-3 gene or antisense oligonucleotide that may target this gene.

One skilled in the art would have no reasonable expectation that the nucleotide sequence provided as Acc. No AAH66886 in the alignment will function as antisense to the BRCC-3 gene that encodes the amino acid sequence of SEQ ID NO:2. Due to the fact that the genetic code is degenerate, one of ordinary skill can not reasonably predict the exact nucleotide sequence that encodes a particular amino acid sequence. Therefore, the Applicants respectfully submit that Claim 23 is non-obvious in view of Schlegel because it is impossible to predict with any degree of certainty that the nucleotide sequence disclosed therein would act as a functional antisense to the gene that encodes the amino acid of SEQ ID NO:2.

Furthermore, it is highly unlikely that the sequence provided as Acc. No AAH66886 in the alignment will function as antisense to the BRCC-3 gene. Antisense oligonucleotides correspond to the sequence of the coding strand from 5' to 3' and compliment the transcribed mRNA. However, the sequence disclosed in Schlegal appears to be provided in 3' to 5' order, based on the numbers indicating the position of the nucleotides on the AAH66886 sequence in the alignment (*i.e.* 124 to 14, rather than 14 to 124). Therefore, Claim 23 is neither anticipated by nor obvious in view of the disclosure of Schlegel because one skilled in the art would not reasonably expect that oligonucleotide with an inverted directional orientation would hybridize to the target correctly and result in a functional antisense molecule.

Furthermore, prior to the Applicants' submission of the BRCC-3 gene data to the GenBank database, the sequence and role of the full-length gene was not yet known. Indeed, the only available sequence data prior to this application comprises a truncated sequence, which is identified as "unnamed DNA." In light of the lack of knowledge of the sequence and function of the full-length gene, one skilled in the art would not be motivated to attempt to engineer an antisense oligonucleotide to the BRCC-3 gene from the sequence provided in Schlegel et al. Thus, an antisense oligonucleotide to the BRCC-3 gene is non-obvious.

Based on the foregoing, Claim 23 can neither be anticipated in view of this non-enabling document nor made obvious without sufficient motivation. The Applicants respectfully request withdrawal of the rejection.

Claims 1-12 and 24 stand rejected under 35 U.S.C. 103(a) as obvious over Gokhale in view of Huang. Huang does not teach the BRCC-3 polynucleotide or amino acid sequence. The rejection relies upon Huang as teaching routine procedures, such as the insertion of a polynucleotide into vector, transformation or transfection of a recombinant host cell, antisense for inhibiting expression of a target gene, and liposomal formulations for delivery of nucleic acids into a host cell. The rejection asserts that, in view of the teachings of Huang, the disclosure of the polynucleotide of SEQ ID NO: 1 by Gokhale renders the Claims 1-12 and 24 obvious.

As discussed above, Gokhale was not publicly available until after the parent application of this application case was filed. Thus, Gokhale does not constitute prior art. Furthermore, polynucleotide sequences can not be predicted or known prior to isolation and sequencing. Therefore, without full disclosure of the sequence data, one skilled in the art could neither make or use the polynucleotides according to the teachings of generic experimental procedures in Huang. Accordingly, the claims, which recite a specific polynucleotide sequence, can not be obvious in view of Huang. Applicants respectfully request withdrawal of the rejection.

In light of the foregoing, the Applicants respectfully submit that the entire Application is now in condition for allowance, which is respectfully requested.

Respectfully submitted,

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Gutjahr, Chai Leng

From: gb-admin@ncbi.nlm.nih.gov
Sent: Monday, July 02, 2001 4:23 PM
To: kasidu@gunet.georgetown.edu
Subject: [NCBI_REF 877226] GenBank AF303178,AF30317

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SEP 24 2007
PATENT & TRADEMARK OFFICE

Dear GenBank Submitter:

Thank you for your submission.

Based on the data submitted to us, the scheduled release date for your submission is:

Oct 1 2001

However, if the accession number is published prior to that date, the sequence will be released upon publication.

Note that the entire sequence will be released when the article citing this accession number is published. If this is not what you intended, please notify us immediately so that we can discuss your submission in more detail.

If this date is not correct, please get in touch with us as soon as possible (gb-admin@ncbi.nlm.nih.gov, telephone at (301) 496-2475, or fax at (301) 480-2918), otherwise this submission will be released on the date indicated above. The data would then be available over the network data servers which provide daily updates of GenBank data. The data are simultaneously made available to EMBL in Europe and the DNA Data Bank of Japan.

Minor changes may have been made in your original submission in order to conform to database annotation conventions. You can greatly assist us in presenting your data in as accurate a manner as possible by paying specific attention to the following in your review:

- Spelling (particularly author names)
- Citation data (author order, page span, etc.)
- Nomenclature ('official' gene names, product labels, etc.)
- Taxonomic and source data
- Feature spans and descriptions (particularly non-coding regions)

Whenever you have additional information about your sequence or if you wish to make revisions, please inform us. Revisions to your data may pertain to the bibliography (e.g., conversion from unpublished to published), the biological data (e.g., new features), or to the sequence data themselves. Please use the following e-mail address:

gb-admin@ncbi.nlm.nih.gov

An accession number has been assigned to each sequence and was provided to you at the time receipt of your submission was acknowledged. We strongly recommend that this number appear in any publication which reports or discusses these data, as it gives the community a convenient label with which they may retrieve your data from our on-line servers.

Thank you once again for your submission.

Respectfully,

Leigh A. Riley, Ph.D.
GenBank Direct Submission Staff
gb-admin@ncbi.nlm.nih.gov

GenBank flat file:

```
LOCUS       AF303178     2468 bp    mRNA            PRI       01-OCT-2001
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  AUTHORS   Gokhale,P.C., Kumar,D., Monia,B.P., Rahman,A., Dritschilo,A. and
            Kasid,U.
  TITLE     Novel Transcript in Human Breast Cancer Cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2468)
  AUTHORS   Gokhale,P.C., Rahman,A., Dritschilo,A. and Kasid,U.
  TITLE     Direct Submission
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REFERENCE   1  (bases 1 to 862)
  AUTHORS   Gokhale,P.C., Kumar,D., Monia,B.P., Rahman,A., Dritschilo,A. and
            Kasid,U.
  TITLE     Novel Transcript in Human Breast Cancer Cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 862)
  AUTHORS   Gokhale,P.C., Rahman,A., Dritschilo,A. and Kasid,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2000) Radiation Medicine, Georgetown University,
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